RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/563,655
Source: IFW
Date Processed by STIC: 1/18/06

ENTERED

IFWP

RAW SEQUENCE LISTING DATE: 01/18/2006
PATENT APPLICATION: **US/10/563,655** TIME: 15:21:28

Input Set : **A:\54-000410US.ST25.txt**
Output Set: **N:\CRF4\01182006\J563655.raw**

<110> APPLICANT: The Scripps Research Institute
Anderson, J C
Schultz, Peter G
<120> TITLE OF INVENTION: COMPOSITIONS OF ORTHOGONAL LEUCYL-tRNA AND AMINOACYL-tRNA SYNTHETASE PAIRS AND USES THEREOF
<130> FILE REFERENCE: 54-000410PC
C--> **<140> CURRENT APPLICATION NUMBER: US/10/563,655**
C--> **<141> CURRENT FILING DATE: 2006-01-05**
<160> NUMBER OF SEQ ID NOS: 72
<170> SOFTWARE: PatentIn version 3.2
<210> SEQ ID NO: 1
<211> LENGTH: 88
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: mutant tRNA
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gagggttcga atcccttccc tcgcacca 88
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<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: mutant tRNA
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gagggttcga atcccttccc tcgcacca 88
<210> SEQ ID NO: 3
<211> LENGTH: 88
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: mutant tRNA
<400> SEQUENCE: 3
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gagggttcga atcccttccc tgggacca 88
<210> SEQ ID NO: 4
<211> LENGTH: 89
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
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69 <400> SEQUENCE: 4
70 gcgagggtag ccaagctcgg ccaacggcga cggacttcct aatccgttct cgtaggagtt 60
72 cgagggttcg aatcccttcc ctcgcacca 89
75 <210> SEQ ID NO: 5
76 <211> LENGTH: 89
77 <212> TYPE: DNA
78 <213> ORGANISM: artificial
80 <220> FEATURE:
81 <223> OTHER INFORMATION: mutant tRNA
83 <400> SEQUENCE: 5
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86 cgagggttcg aatccctccc ctcgcacca 89
89 <210> SEQ ID NO: 6
90 <211> LENGTH: 89
91 <212> TYPE: DNA
92 <213> ORGANISM: artificial
94 <220> FEATURE:
95 <223> OTHER INFORMATION: mutant tRNA
97 <400> SEQUENCE: 6
98 gcgggggttg ccgagcctgg ccaaaggcgc cggacttcct aatccggtcc cgtaggggtt 60
100 ccggggttca aatccccgcc cccgcacca 89
103 <210> SEQ ID NO: 7
104 <211> LENGTH: 88
105 <212> TYPE: DNA
106 <213> ORGANISM: artificial
108 <220> FEATURE:
109 <223> OTHER INFORMATION: mutant tRNA
111 <400> SEQUENCE: 7
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114 cggggttcaa atccccgccc ccgcacca 88
117 <210> SEQ ID NO: 8
118 <211> LENGTH: 77
119 <212> TYPE: DNA
120 <213> ORGANISM: artificial
122 <220> FEATURE:
123 <223> OTHER INFORMATION: mutant tRNA
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128 tccggcccgc cggacca 77
131 <210> SEQ ID NO: 9
132 <211> LENGTH: 90
133 <212> TYPE: DNA
134 <213> ORGANISM: Escherichia coli
136 <400> SEQUENCE: 9
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142 <210> SEQ ID NO: 10
143 <211> LENGTH: 91
144 <212> TYPE: DNA

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Input Set : A:\54-000410US.ST25.txt
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<220> FEATURE:
<223> OTHER INFORMATION: mutant tRNA
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accgggggtt caaatccccc tctctccgcc a 91
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<211> LENGTH: 88
<212> TYPE: RNA
<213> ORGANISM: Halobacterium sp. NRC-1
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gaggguucga aucccuuccc ucgcacca 88
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<211> LENGTH: 89
<212> TYPE: RNA
<213> ORGANISM: artificial
<220> FEATURE:
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<400> SEQUENCE: 12
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cgggggguuca aaucccccgcc cccgcacca 89
<210> SEQ ID NO: 13
<211> LENGTH: 2799
<212> TYPE: DNA
<213> ORGANISM: Archaeoglobus fulgidus
<400> SEQUENCE: 13
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aatggaaatc ttcacgcagg tcacacgaga accttcacaa ttggcgatgc cttcgccaga 180
tacatgagaa tgaagggcta caacgttctc tttcccctcg gctttcatgt tacgggcacc 240
ccaatcattg gccttgcgga gctcatagcc aagagggacg agaggacgat agaggtttac 300
accaaatacc atgacgttcc gctggaggac ttgcttcagc tcacaactcc agagaaaatc 360
gttgagtact tctcaaggga ggcgctgcag gctttgaaga gcataggcta ctccattgac 420
tggaggaggg ttttcaccac aaccgatgaa gagtatcaga gattcatcga gtggcagtac 480
tggaagctca aggagcttgg cctgattgtg aagggcaccc accccgtcag atactgcccc 540
cacgaccaga atcctgttga agaccacgac cttctcgctg gggaggaggc aactattgtt 600
gaatttaccg ttataaagtt caggcttgaa gatggagacc tcattttccc ctgtgcaact 660
ctccgtcccg aaaccgtgtt tggcgtcacg aacatctggg taaagccgac aacctacgta 720
attgccgagg tggatgggga aaagtggttt gtgagcaaag aggcttacga gaagctcacc 780
tacacggaga aaaaagtcag gctgctggag gaggttgatg cgtcgcagtt cttcggcaag 840
tacgtcatag tcccgctggt aaacagaaaa gtgccaattc tgcctgcaga gtttgttgac 900
accgacaacg caacaggagt tgtgatgagc gttcccgcac acgctccttt tgacctggct 960
gccattgagg acttgaagag agacgaggaa acgctggcga agtacggaat tgacaaaagc 1020
gttgtagaga gcataaagcc aatagttctg attaagacgg acattgaagg tgttcctgct 1080
gagaagctaa taagagagct tggagtgaag agccagaagg acaaggagct gctggataag 1140
gcaaccaaga ccctctacaa gaaggagtac cacacgggaa tcatgctgga caacacgatg 1200
aactatgctg gaatgaaagt ttctgaggcg aaggagagag ttcatgagga tttggttaag 1260
cttggcttgg gggatgtttt ctacgagttc agcgagaagc ccgtaatctg caggtgcgga 1320

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231 acgaagtgcg ttgttaaggt tgttagggac cagtggttcc tgaactactc caacagagag 1380
233 tggaaggaga aggttctgaa tcaccttgaa aagatgcgaa tcatccccga ctactacaag 1440
235 gaggagttca ggaacaagat tgagtggctc agggacaagg cttgtgccag aaggaagggg 1500
237 cttggaacga gaattccgtg ggataaggag tggctcatcg agagcctttc agactcaaca 1560
239 atctacatgg cctactacat ccttgccaag tacatcaacg caggattgct caaggccgag 1620
241 aacatgactc ccgagttcct cgactacgtg ctgctgggca aaggtgaggt tgggaaagtt 1680
243 gcggaagctt caaaactcag cgtggagtta atccagcaga tcagggacga cttcgagtac 1740
245 tggtatcccg ttgacctaag aagcagtggc aaggacttgg ttgcaaacca cctgctcttc 1800
247 tacctcttcc accacgtcgc cattttcccg ccagataagt ggccgagggc aattgccgta 1860
249 aacggatacg tcagccttga gggcaagaag atgagcaaga gcaaagggcc cttgctaacg 1920
251 atgaagaggg cggtgcagca gtatggtgcg gatgtgacga ggctctacat cctccacgct 1980
253 gcagagtacg acagcgatgc ggactggaag agcagagagg ttgaagggct tgcaaaccac 2040
255 ctcaggaggt tctacaacct cgtgaaggag aactacctga aagaggtggg agagctaaca 2100
257 accctcgacc gctggcttgt gagcaggatg cagagggcaa taaaggaagt gagggaggct 2160
259 atggacaacc tgcagacgag gagggccgtg aatgccgcct tcttcgagct catgaacgac 2220
261 gtgagatggt atctgaggag aggaggtgag aacctcgcta taatactgga cgactggatc 2280
263 aagctcctcg ccccctttgc tccgcacatt tgcgaggagc tgtggcactt gaagcatgac 2340
265 agctacgtca gcctcgaaag ctacccagaa tacgacgaaa ccagggttga cgaggaggcg 2400
267 gagagaattg aggaatacct ccgaaacctt gttgaggaca ttcaggaaat caagaagttt 2460
269 gttagcgatg cgaaggaggt ttacattgct cccgccgaag actggaaggt taaggcagca 2520
271 aaggtcgttg ctgaaagcgg ggatgttggg gaggcgatga agcagcttat gcaggacgag 2580
273 gagcttagga agctcggcaa agaagtgtca aatttcgtca agaagatttt caaagacaga 2640
275 aagaagctga tgctagttaa ggagtgggaa gttctgcagc agaacctgaa atttattgag 2700
277 aatgagaccg gactgaaggt tattcttgat actcagagag ttcctgagga gaagaggagg 2760
279 caggcagttc cgggcaagcc cgcgatttat gttgcttaa 2799
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283 <211> LENGTH: 2814
284 <212> TYPE: DNA
285 <213> ORGANISM: Methanobacterium thermoautotrophicum
287 <400> SEQUENCE: 14
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290 cctgatgaca gagaaaagat attcctcaca gtcgcttacc cctaccccag tggtgcgatg 120
292 cacataggac acgggaggac ctacactgtc cctgatgtct atgcacggtt caagaggatg 180
294 cagggctaca acgtcctgtt tcccatggcc tggcatgtca caggggcccc tgtcataggg 240
296 atagcgcgga ggattcagag gaaggatccc tggaccctca aaatctacag ggaggtccac 300
298 agggtccccg aggatgagct tgaacgtttc agtgaccctg agtacatagt tgaatacttc 360
300 agcagggaat accggtctgt tatggaggat atgggctact ccatcgactg gaggcgtgaa 420
302 ttcaaaacca cggatcccac ctacagcagg ttcatacagt ggcagataag gaagctgagg 480
304 gaccttggcc tcgtaaggaa gggcgcccat cctgttaagt actgccctga atgtgaaaac 540
306 cctgtgggtg accatgacct ccttgagggt gaggggttg ccataaacca gctcacactc 600
308 ctcaaattca aacttggaga ctcatacctg gtcgcagcca ccttcaggcc cgagacaatc 660
310 tatggggcca ccaacctctg gctgaaccct gatgaggatt atgtgagggt tgaaacaggt 720
312 ggtgaggagt ggataataag cagggctgcc gtggataatc tttcacacca gaaactggac 780
314 ctcaaggttt ccggtgacgt caaccccggg gacctgatag ggatgtgcgt ggagaatcct 840
316 gtgacgggcc aggaacaccc catactcccg gcttccttcg ttgaccctga atatgccaca 900
318 ggtgttgtgt tctctgtccc tgcacatgcc cctgcagact tcatagccct tgaggacctc 960
320 aggacagacc atgaactcct tgaaaggtac ggtcttgagg atgtggttgc tgatattgag 1020
322 cccgtgaatg tcatagcagt ggatggctac ggtgagttcc cggcggccga ggttatagag 1080
324 aaatttggtg tcagaaacca ggaggacccc cgccttgagg atgccaccgg ggagctatac 1140

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Output Set: **N:\CRF4\01182006\J563655.raw**

326 aagatcgagc atgcgagggg tgttatgagc agccacatcc ctgtctatgg tggtatgaag 1200
328 gtctctgagg cccgtgaggt catcgctgat gaactgaagg accagggcct tgcagatgag 1260
330 atgtatgaat tcgctgagcg acctgttata tgccgctgcg gtggcaggtg cgttgtgagg 1320
332 gtcatggagg accagtggtt catgaagtac tctgatgacg cctggaagga cctcgcccac 1380
334 aggtgcctcg atggcatgaa gataataccc gaggaggtcc gggccaactt tgaatactac 1440
336 atcgactggc tcaatgactg ggcatgttca aggaggatag gccttggaac aaggctgccc 1500
338 tgggatgaga ggtggatcat cgaacccctc acagactcaa caatctacat ggcatattac 1560
340 accatcgcac accgcctcag ggagatggat gccggggaga tggacgatga gttctttgat 1620
342 gccatattcc tagatgattc aggaaccttt gaggatctca gggaggaatt ccggtactgg 1680
344 taccccttg actggaggct ctctgcaaag gacctcatag gcaatcacct gacattccat 1740
346 atattccacc actcagccat attccctgag tcagggtggc cccgggggc tgtggtcttt 1800
348 ggtatgggcc ttcttgaggg caacaagatg tcatcctcca agggcaacgt catactcctg 1860
350 agggatgcca tcgagaagca cggtgcagac gtggtgcggc tcttcctcat gtcctcagca 1920
352 gagccatggc aggactttga ctggagggag agtgaggtca tcgggacccg caggaggatt 1980
354 gaatggttca gggaattcgg agagagggtc tcaggtatcc tggatggtag gccagtcctc 2040
356 agtgaggtta ctccagctga acctgaaagc ttcattggaa ggtggatgat gggtcagctg 2100
358 aaccagagga tacgtgaagc cacaagggcc cttgaatcat tccagacaag aaaggcagtt 2160
360 caggaggcac tctatctcct taaaaaggat gttgaccact accttaagcg tgttgagggt 2220
362 agagttgatg atgaggttaa atctgtcctt gcaaacgttc tgcacgcctg gataaggctc 2280
364 atggctccat tcatacccta cactgctgag gagatgtggg agaggtatgg tggtgagggt 2340
366 tttgtagcag aagctccatg gcctgacttc tcagatgatg cagagagcag ggatgtgcag 2400
368 gttgcagagg agatggtcca gaataccgtt agagacattc aggaaatcat gaagatcctt 2460
370 ggatccaccc cggagagggt ccacatatac acctcaccaa aatggaaatg ggatgtgcta 2520
372 agggtcgcag cagaggtagg aaaactagat atgggctcca taatgggaag ggtttcagct 2580
374 gagggcatcc atgataacat gaaggaggtt gctgaatttg taaggaggat catcagggac 2640
376 cttggtaaat cagaggttac ggtgatagac gagtacagcg tactcatgga tgcatctgat 2700
378 tacattgaat cagaggttgg agccagggtt gtgatacaca gcaaaccaga ctatgaccct 2760
380 gaaaacaagg ctgtgaatgc cgttcccctg aagccagcca tataccttga atga 2814
383 <210> SEQ ID NO: 15
384 <211> LENGTH: 932
385 <212> TYPE: PRT
386 <213> ORGANISM: Archaeoglobus fulgidus
388 <400> SEQUENCE: 15
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391 1 5 10 15
394 Lys Asp Arg Ile Phe Glu Ser Asp Pro Asn Glu Lys Glu Lys Phe Phe
395 20 25 30
398 Leu Thr Ile Pro Tyr Pro Tyr Leu Asn Gly Asn Leu His Ala Gly His
399 35 40 45
402 Thr Arg Thr Phe Thr Ile Gly Asp Ala Phe Ala Arg Tyr Met Arg Met
403 50 55 60
406 Lys Gly Tyr Asn Val Leu Phe Pro Leu Gly Phe His Val Thr Gly Thr
407 65 70 75 80
410 Pro Ile Ile Gly Leu Ala Glu Leu Ile Ala Lys Arg Asp Glu Arg Thr
411 85 90 95
414 Ile Glu Val Tyr Thr Lys Tyr His Asp Val Pro Leu Glu Asp Leu Leu
415 100 105 110
418 Gln Leu Thr Thr Pro Glu Lys Ile Val Glu Tyr Phe Ser Arg Glu Ala
419 115 120 125

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 01/18/2006
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Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:17; N Pos. 3750,3770
Seq#:18; N Pos. 3749,3769
Seq#:19; N Pos. 3749,3769
Seq#:20; N Pos. 3274,3294
Seq#:72; N Pos. 31,45,77

Invalid <213> Response:
Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1,2,3,4,5,6,7,8,10,12,17,18,19,20,21,23,24,25,26,27,28,29,30,31,32,33,34
Seq#:35,36,72

VERIFICATION SUMMARY DATE: 01/18/2006
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L:12 M:270 C: Current Application Number differs, Replaced Current Application Number
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:1013 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:3720
L:1196 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:3720
L:1379 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:3720
L:1546 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20 after pos.:3240
L:2260 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:72 after pos.:0
M:341 Repeated in SeqNo=72